

SEQUENCE LISTING

<110> Lindquist, Susan
Li, Liming
Ma, Jiyan
Liu, Jia-Jia
Sondheimer, Neal
Scheibel, Thomas

<120> RECOMBINANT PRION-LIKE GENES AND PROTEINS AND MATERIALS
AND METHODS COMPRISING SAME

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<151> 1999-06-09

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<170> PatentIn Ver. 2.0

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Ser	Asn	Ile	Asn	Phe	Glu	Phe	Ser	Thr	Gly	Val	Asn	Asn	Asn	Asn	Asn
		35					40					45			
Asn	Asn	Ser	Ser	Ser	Asn	Asn	Asn	Asn	Val	Gln	Asn	Asn	Asn	Ser	Gly
		50				55					60				
Arg	Asn	Gly	Ser	Gln	Asn	Asn	Asp	Asn	Glu	Asn	Asn	Ile	Lys	Asn	Thr
65					70					75					80
Leu	Glu	Gln	His	Arg	Gln	Gln	Gln	Gln	Ala	Phe	Ser	Asp	Met	Ser	His
				85					90					95	
Val	Glu	Tyr	Ser	Arg	Ile	Thr	Lys	Phe	Phe	Gln	Glu	Gln	Pro	Leu	Glu
			100					105					110		
Gly	Tyr	Thr	Leu	Phe	Ser	His	Arg	Ser	Ala	Pro	Asn	Gly	Phe	Lys	Val
		115					120					125			
Ala	Ile	Val	Leu	Ser	Glu	Leu	Gly	Phe	His	Tyr	Asn	Thr	Ile	Phe	Leu
		130				135					140				
Asp	Phe	Asn	Leu	Gly	Glu	His	Arg	Ala	Pro	Glu	Phe	Val	Ser	Val	Asn
145					150					155					160
Pro	Asn	Ala	Arg	Val	Pro	Ala	Leu	Ile	Asp	His	Gly	Met	Asp	Asn	Leu
				165					170					175	
Ser	Ile	Trp	Glu	Ser	Gly	Ala	Ile	Leu	Leu	His	Leu	Val	Asn	Lys	Tyr
			180					185					190		
Tyr	Lys	Glu	Thr	Gly	Asn	Pro	Leu	Leu	Trp	Ser	Asp	Asp	Leu	Ala	Asp
		195					200					205			
Gln	Ser	Gln	Ile	Asn	Ala	Trp	Leu	Phe	Phe	Gln	Thr	Ser	Gly	His	Ala
	210					215					220				
Pro	Met	Ile	Gly	Gln	Ala	Leu	His	Phe	Arg	Tyr	Phe	His	Ser	Gln	Lys
225					230					235					240
Ile	Ala	Ser	Ala	Val	Glu	Arg	Tyr	Thr	Asp	Glu	Val	Arg	Arg	Val	Tyr
				245					250					255	
Gly	Val	Val	Glu	Met	Ala	Leu	Ala	Glu	Arg	Arg	Glu	Ala	Leu	Val	Met
			260					265					270		
Glu	Leu	Asp	Thr	Glu	Asn	Ala	Ala	Ala	Tyr	Ser	Ala	Gly	Thr	Thr	Pro
		275					280					285			
Met	Ser	Gln	Ser	Arg	Phe	Phe	Asp	Tyr	Pro	Val	Trp	Leu	Val	Gly	Asp
	290					295					300				
Lys	Leu	Thr	Ile	Ala	Asp	Leu	Ala	Phe	Val	Pro	Trp	Asn	Asn	Val	Val

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<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FLAG peptide

<400> 5
Asp Tyr Lys Asp Asp Asp Lys
 1             5

<210> 6
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FLAG peptide

<400> 6
Asp Tyr Lys Asp Glu Asp Asp Lys
 1             5

<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Strep epitope

<400> 7
Ala Trp Arg His Pro Gln Phe Gly Gly
 1             5

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hemagglutinin
      epitope

<400> 8
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ile Glu Gly Arg
 1             5             10

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<400> 12
atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
gatgttaatg gtcacaaatt ttctgtctcc ggtgaagggtg aagggtgatgc tacttacggt 120
aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
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<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence
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<400> 13
tacccatagc acgtcccaga ctacgct 27

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<220>  
<221> CDS  
<222> (1) .. (645)
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<400>	14															
atg	tcg	gat	tca	aac	caa	ggc	aac	aat	cag	caa	aac	tac	cag	caa	tac	48
Met	Ser	Asp	Ser	Asn	Gln	Gly	Asn	Asn	Gln	Gln	Asn	Tyr	Gln	Gln	Tyr	
1				5					10					15		
<hr/>																
agc	cag	aac	ggg	aac	caa	caa	caa	ggg	aac	aac	aga	tac	caa	ggg	tac	96
Ser	Gln	Asn	Gly	Asn	Gln	Gln	Gln	Gly	Asn	Asn	Arg	Tyr	Gln	Gly	Tyr	
			20					25					30			
<hr/>																
caa	gct	tac	aat	gct	caa	gcc	caa	cct	gca	ggg	ggg	tac	tac	caa	aac	144
Gln	Ala	Tyr	Asn	Ala	Gln	Ala	Gln	Pro	Ala	Gly	Gly	Tyr	Tyr	Gln	Asn	
		35					40					45				
<hr/>																
tac	caa	ggg	tac	tct	ggg	tac	cca	caa	ggg	ggg	cgt	gga	aac	tac	aaa	192
Tyr	Gln	Gly	Tyr	Ser	Gly	Tyr	Pro	Gln	Gly	Gly	Arg	Gly	Asn	Tyr	Lys	
	50					55					60					
<hr/>																
aac	ttc	aac	tac	aac	aac	aac	ttg	caa	gga	tac	caa	gct	ggg	ttc	caa	240
Asn	Phe	Asn	Tyr	Asn	Asn	Asn	Leu	Gln	Gly	Tyr	Gln	Ala	Gly	Phe	Gln	
65					70					75				80		

Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser
100 105 110

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<210> 16
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: yeast
      Sup35R2E2 encoding sequence

<220>
<221> CDS
<222> (1)..(813)

<400> 16
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac    48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
  1              5              10              15

agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat    96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
              20              25              30

caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat    144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
              35              40              45

tac caa ggt tat tct ggg tac caa caa ggt ggc tat caa cag tac aat    192
Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
  50              55              60

ccc caa ggt ggc tat caa cag tac aat ccc caa ggt ggc tat caa cag    240
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
  65              70              75              80

tac aat ccc gac gcc ggt tac cag caa cag tat aat cct caa gga ggc    288
Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly
              85              90              95

tat caa cag tac aat cct caa ggc ggt tat cag cag caa ttc aat cca    336
Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
              100              105              110

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caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat aac aat ttg	384
Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu	
115 120 125	
caa gga tat caa gct ggt ttc caa cca cag tct caa ggt atg tct ttg	432
Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu	
130 135 140	
aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa cca aag aag	480
Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys	
145 150 155 160	
act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc aat gct acc	528
Thr Leu Lys Leu Val Ser Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr	
165 170 175	
aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa gag gaa gag	576
Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu	
180 185 190	
aag tct gct gaa acc aaa gaa cca act aaa gag cca aca aag gtc gaa	624
Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu	
195 200 205	
gaa cca gtt aaa aag gag gag aaa cca gtc cag act gaa gaa aag acg	672
Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr	
210 215 220	
gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa atc tct gaa	720
Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu	
225 230 235 240	
tca aca cat aat acc aac aat gcc aat gtt acc agt gct gat gcc ttg	768
Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu	
245 250 255	
atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt aac gat	813
Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp	
260 265 270	

<210> 17

<211> 271

<212> PRT

<213> Artificial Sequence

<400> 17

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr

1

5

10

15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr

20

25

30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn

35

40

45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn

50

55

60

Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln

65

70

75

80

Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly

<210>	18
<211>	641
<212>	DNA
<213>	MOUSE

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<220>  
<221> CDS  
<222> (1) .. (633)
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Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser	
1				5				10				15				
cgg	tat	ccc	ggg	cag	gga	agc	cct	gga	ggc	aac	cgt	tac	cca	cct	cag	96
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln	
20				25				30								
ggt	ggc	acc	tgg	ggg	cag	ccc	cac	ggt	ggt	ggc	tgg	gga	caa	ccc	cat	144
Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	
35				40				45								
ggg	ggc	agc	tgg	gga	caa	cct	cat	ggt	ggt	agt	tgg	ggt	cag	ccc	cat	192
Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	
50				55				60								
ggc	ggt	gga	tgg	ggc	caa	gga	ggg	ggt	acc	cat	aat	cag	tgg	aac	aag	240

Gly	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His	Asn	Gln	Trp	Asn	Lys	
65					70					75					80	
ccc	agc	aaa	cca	aaa	acc	aac	ctc	aag	cat	gtg	gca	ggg	gct	gcg	gca	288
Pro	Ser	Lys	Pro	Lys	Thr	Asn	Leu	Lys	His	Val	Ala	Gly	Ala	Ala	Ala	
				85					90					95		
gct	ggg	gca	gta	gtg	ggg	ggc	ctt	ggg	ggc	tac	atg	ctg	ggg	agc	gcc	336
Ala	Gly	Ala	Val	Val	Gly	Gly	Leu	Gly	Gly	Tyr	Met	Leu	Gly	Ser	Ala	
			100					105					110			
gtg	agc	agg	ccc	atg	atc	cat	ttt	ggc	aac	gac	tgg	gag	gac	cgc	tac	384
Val	Ser	Arg	Pro	Met	Ile	His	Phe	Gly	Asn	Asp	Trp	Glu	Asp	Arg	Tyr	
		115					120					125				
tac	cgt	gaa	aac	atg	tac	cgc	tac	cct	aac	caa	gtg	tac	tac	agg	cca	432
Tyr	Arg	Glu	Asn	Met	Tyr	Arg	Tyr	Pro	Asn	Gln	Val	Tyr	Tyr	Arg	Pro	
	130					135					140					
gtg	gat	cag	tac	agc	aac	cag	aac	aac	ttc	gtg	cac	gac	tgc	gtc	aat	480
Val	Asp	Gln	Tyr	Ser	Asn	Gln	Asn	Asn	Phe	Val	His	Asp	Cys	Val	Asn	
145					150					155					160	
atc	acc	atc	aag	cag	cac	acg	gtc	acc	acc	acc	acc	aag	ggg	gag	aac	528
Ile	Thr	Ile	Lys	Gln	His	Thr	Val	Thr	Thr	Thr	Thr	Lys	Gly	Glu	Asn	
				165				170						175		
ttc	acc	gag	acc	gat	gtg	aag	atg	atg	gag	cgc	gtg	gtg	gag	cag	atg	576
Phe	Thr	Glu	Thr	Asp	Val	Lys	Met	Met	Glu	Arg	Val	Val	Glu	Gln	Met	
			180				185						190			
tgc	gtc	acc	cag	tac	cag	aag	gag	tcc	cag	gcc	tat	tac	gac	ggg	aga	624
Cys	Val	Thr	Gln	Tyr	Gln	Lys	Glu	Ser	Gln	Ala	Tyr	Tyr	Asp	Gly	Arg	
		195					200					205				
aga	tcc	agc	tgataacc													641
Arg	Ser	Ser														
		210														
<210>	19															
<211>	211															
<212>	PRT															
<213>	MOUSE															
<400>	19															
Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser	
1				5					10					15		
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln	
			20					25					30			
Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	
		35					40					45				
Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	
		50				55					60					
Gly	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His	Asn	Gln	Trp	Asn	Lys	
65					70					75					80	
Pro	Ser	Lys	Pro	Lys	Thr	Asn	Leu	Lys	His	Val	Ala	Gly	Ala	Ala	Ala	
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<210> 20
<211> 644
<212> DNA
<213> Mesocricetus auratus
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<400> 20																	
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Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser		
1				5				10					15				
cga	tac	cct	ggg	cag	ggc	agc	cct	gga	ggc	aac	cgt	tac	cca	cct	cag	96	
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln		
			20					25					30				
ggt	ggc	ggc	aca	tgg	ggg	caa	ccc	cat	ggt	ggt	ggc	tgg	gga	cag	ccc	144	
Gly	Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro		
		35					40					45					
cat	ggt	ggt	ggc	tgg	gga	cag	ccc	cat	ggt	ggt	ggc	tgg	ggt	cag	ccc	192	
His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro		
	50					55					60						
cat	ggt	ggt	ggc	tgg	ggt	caa	gga	ggt	ggc	acc	cac	aat	cag	tgg	aac	240	
His	Gly	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His	Asn	Gln	Trp	Asn		
	65				70					75					80		
aag	ccc	agt	aag	cca	aaa	acc	aac	atg	aag	cac	atg	gcc	ggc	gct	gct	288	
Lys	Pro	Ser	Lys	Pro	Lys	Thr	Asn	Met	Lys	His	Met	Ala	Gly	Ala	Ala		
				85					90					95			
gcg	gca	ggg	gcc	gtg	gtg	ggg	ggc	ctt	ggt	ggc	tac	atg	ctg	ggg	agt	336	
Ala	Ala	Gly	Ala	Val	Val	Gly	Gly	Leu	Gly	Gly	Tyr	Met	Leu	Gly	Ser		
			100					105					110				

Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val

<210> 22
<211> 780
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 22
Met Lys Lys Lys Asp Asn Ser Asp Asp Lys Asp Asn Val Ala Ser Gly
1 5 10 15
Gly Tyr Lys Asn Ala Ala Asp Ala Gly Ser Asn Asn Ala Ser Lys Lys
20 25 30
Ser Ser Tyr Arg Asn Trp Lys Gly Gly Asn Tyr Gly Gly Tyr Ser Tyr
35 40 45
Asn Ser Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr
50 55 60
Asn Asn Tyr Asn Asn Tyr Asn Lys Tyr Asn Gly Gly Tyr Lys Ser Thr
65 70 75 80
Tyr Lys Ser Ala Val Thr Asn Ser Gly Thr Thr Ser Ala Ser Thr Thr
85 90 95
Ser Thr Ser Asn Lys Ser Asn Thr Ser Ser Lys Cys Ser Thr Asp Cys
100 105 110
Lys Asn Lys Gly Lys Gly Asn Ser Thr Gly Lys Trp Lys Val Asp Val
115 120 125
Ser Lys Lys Lys Asn Ser Val Arg Ser Ala Met Ser Asn Ala Ser Gly
130 135 140
Lys Ala Tyr Asn Val Ala Asp Cys Ser Asp Lys Asn Thr Val Lys Arg
145 150 155 160
Ala Ala His Ala Asp Ser Asn Cys Met Ala Thr Cys Val Thr Asp Tyr
165 170 175
Ser Ser Gly Ala Lys Trp Ala Lys Met Ala Ala Ser Val Val Asp Arg
180 185 190
Arg Asp Ser Ala Asn Asp Thr Lys Asp Ala Val Val Thr Asp Val Ala
195 200 205
Thr Asp Lys Ala Lys Gly Tyr Lys Thr Asp Tyr Val Ser Asp Asn Asp
210 215 220

Ser 225	Arg	Tyr	Lys	Val	Asp 230	Thr	Asp	Ser	Lys	Val	Ser	Val	Lys	Ser	Ser 240
Ser	Val	Thr	Val	Ala 245	Val	Thr	Ser	Ser	Val 250	Asn	Arg	Ser	Asn	Ser 255	Ser
Ser	Ser	Arg	Thr 260	Val	Val	Val	Asn	Thr 265	Arg	Val	Asn	Asn	Arg 270	Asn	Ser
Gly	Lys	Val	Val	Asp	Thr	Ala	Ser 280	Val	Arg	Ala	Lys	Ala 285	Asn	Val	Lys
Asp	Asp 290	Ala	Asp	Lys	Asn	Lys 295	Ser	Gly	Arg	Thr	Gly 300	Arg	Asp	Asp	His
Lys 305	Asp	Lys	Ala	Asp	Asp 310	Ser	Cys	Val	Lys	Tyr 315	Met	Asn	Asp	Thr	Val 320
Lys	Tyr	Met	Ser	Lys 325	Thr	Val	Asp	Ser	Asn 330	Val	Asn	Asp	Trp	Lys 335	Arg
Asp	Thr	Ala	Val 340	Gly	Gly	Ser	Asp 345	Ser	Arg	Val	Lys	Asp	His 350	Asn	Arg
Ala	Tyr	Lys 355	Arg	Ala	Asp	Asp	Gly 360	Val	Asn	Thr	Asp	Ser 365	Ala	Tyr	Gly
Ser	Arg 370	Met	Asn	Lys	Thr	Asn 375	Arg	Lys	Gly	His	Arg 380	Tyr	Gly	Cys	Gly
Arg 385	Asn	Gly	Ala	Gly	Lys 390	Ser	Thr	Met	Arg	Ala 395	Ala	Asn	Gly	Asp	Gly 400
Asp	Lys	Asp	Thr	Arg 405	Thr	Cys	Val	His	Lys 410	Gly	Gly	Asp	Asp	Val 415	Ser
Ala	Asp	Ser	Thr 420	Ser	Arg	Ala	Ala 425	Ala	Ser	Val	Gly	Asp	Arg 430	Arg	Ala
Thr	Val	Gly 435	Ser	Ser	Gly	Gly	Trp 440	Lys	Met	Lys	Ala	Arg 445	Ala	Met	Lys
Ala	Asp 450	Asp	Thr	Asn	His	Asp 455	Val	Ser	Asn	Val	Lys 460	Trp	Tyr	His	Thr
Asp 465	Thr	Ser	Val	Ser	His 470	Asp	Ser	Gly	Asp	Thr 475	Val	Cys	Thr	Asp	His 480
Tyr	Asn	Lys	Lys	Ala 485	Tyr	Tyr	Lys	Gly	Asn 490	Ala	Ala	Val	Lys	Ala 495	Lys
Ser	Tyr	Tyr	Thr 500	Thr	Asp	Ser	Asn	Ala 505	Met	Arg	Gly	Thr	Gly 510	Val	Lys
Ser	Asn	Thr 515	Arg	Ala	Val	Ala	Lys 520	Met	Thr	Asp	Val	Thr 525	Ser	Tyr	Gly
Ala	Lys 530	Ser	Ser	His	Val	Ser 535	Cys	Ser	Ser	Ser	Ser 540	Arg	Val	Ala	Cys
Gly 545	Asn	Gly	Ala	Gly	Lys 550	Ser	Thr	Lys	Thr	Gly 555	Val	Asn	Gly	Lys	Val 560

Lys His Asn Arg Gly Tyr Ala His Ala His Val Asn His Lys Lys Thr
565 570 575

Ala Asn Tyr Trp Arg Tyr Gly Asp Asp Arg Val Lys Ser Arg Lys Ser
580 585 590

Asp Lys Met Met Thr Lys Asp Asp Asp Gly Arg Gly Lys Arg Ala Ala
595 600 605

Val Gly Arg Lys Lys Lys Ser Tyr Val Lys Trp Lys Tyr Trp Lys Lys
610 615 620

Tyr Asn Ser Trp Val Lys Asp Val Val His Gly Lys Val Lys Asp Asp
625 630 635 640

His Ala Ser Arg Gly Gly Tyr Arg Ser Val Thr Lys His Asp Val Gly
645 650 655

Asp Ser Ala Asn His Thr Gly Ser Ser Gly Gly Val Lys Val Val Ala
660 665 670

Gly Ala Met Trp Asn Asn His Val Asp Thr Asn Tyr Asp Arg Asp Ser
675 680 685

Gly Ala Ala Val Ala Arg Asp Trp Ser Gly Gly Val Val Met Ser His
690 695 700

Asn Asn Val Gly Ala Cys Trp Val Asn Gly Lys Met Val Lys Gly Ser
705 710 715 720

Ala Val Asp Ser Lys Asp Gly Gly Asn Ala Asp Ala Val Gly Lys Ala
725 730 735

Ser Asn Ala Lys Ser Val Asp Asp Asp Asp Ser Ala Asn Lys Val Lys
740 745 750

Arg Lys Lys Arg Thr Arg Asn Lys Lys Ala Arg Arg Arg Arg Tyr Trp
755 760 765

Ser Ser Lys Gly Thr Lys Val Asp Thr Asp Asp Asp
770 775 780

<210> 23

<211> 1075

<212> PRT

<213> Saccharomyces cerevisiae

<400> 23

Met Asp Asn Lys Arg Leu Tyr Asn Gly Asn Leu Ser Asn Ile Pro Glu
1 5 10 15

Val Ile Asp Pro Gly Ile Thr Ile Pro Ile Tyr Glu Glu Asp Ile Arg
20 25 30

Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val Ser Asp
35 40 45

Lys Arg Gly Arg Ser Ser Ser Thr Ser Pro Gln Lys Ile Gly Ser Tyr
50 55 60

Arg Thr Arg Ala Gly Arg Phe Ser Asp Thr Leu Thr Asn Leu Leu Pro
65 70 75 80

Ser	Ile	Ser	Ala	Lys 85	Leu	His	His	Ser	Lys 90	Lys	Ser	Thr	Pro	Val 95	Val
Val	Val	Pro	Pro 100	Thr	Ser	Ser	Thr	Pro 105	Asp	Ser	Leu	Asn	Ser 110	Thr	Thr
Tyr	Ala	Pro 115	Arg	Val	Ser	Ser	Asp 120	Ser	Phe	Thr	Val	Ala 125	Thr	Pro	Leu
Ser	Leu 130	Gln	Ser	Thr	Thr	Thr 135	Arg	Thr	Arg	Thr	Arg 140	Asn	Asn	Thr	Val
Ser 145	Ser	Gln	Ile	Thr 150	Ala	Ser	Ser	Ser	Leu	Thr 155	Thr	Asp	Val	Gly	Asn 160
Ala	Thr	Ser	Ala	Asn 165	Ile	Trp	Ser	Ala	Asn 170	Ala	Glu	Ser	Asn	Thr 175	Ser
Ser	Ser	Pro	Leu 180	Phe	Asp	Tyr	Pro	Leu 185	Ala	Thr	Ser	Tyr	Phe 190	Glu	Pro
Leu	Thr	Arg 195	Phe	Lys	Ser	Thr	Asp 200	Asn	Tyr	Thr	Leu	Pro 205	Gln	Thr	Ala
Gln	Leu 210	Asn	Ser	Phe	Leu	Glu 215	Lys	Asn	Gly	Asn	Pro 220	Asn	Ile	Trp	Ser
Ser 225	Ala	Gly	Asn	Ser	Asn 230	Thr	Asp	His	Leu	Asn 235	Thr	Pro	Ile	Val	Asn 240
Arg	Gln	Arg	Ser	Gln 245	Ser	Gln	Ser	Thr	Thr 250	Asn	Arg	Val	Tyr	Thr 255	Asp
Ala	Pro	Tyr	Tyr 260	Gln	Gln	Pro	Ala	Gln 265	Asn	Tyr	Gln	Val	Gln 270	Val	Pro
Pro	Arg	Val 275	Pro	Lys	Ser	Thr	Ser 280	Ile	Ser	Pro	Val	Ile 285	Leu	Asp	Asp
Val	Asp 290	Pro	Ala	Ser	Ile	Asn 295	Trp	Ile	Thr	Ala	Asn 300	Gln	Lys	Val	Pro
Leu 305	Val	Asn	Gln	Ile	Ser 310	Ala	Leu	Leu	Pro	Thr 315	Asn	Thr	Ile	Ser	Ile 320
Ser	Asn	Val	Phe	Pro 325	Leu	Gln	Pro	Thr	Gln 330	Gln	His	Gln	Gln	Asn 335	Ala
Val	Asn	Leu	Thr 340	Ser	Thr	Ser	Leu	Ala 345	Thr	Leu	Cys	Ser	Gln 350	Tyr	Gly
Lys	Val	Leu 355	Ser	Ala	Arg	Thr	Leu 360	Arg	Gly	Leu	Asn	Met 365	Ala	Leu	Val
Glu	Phe 370	Ser	Thr	Val	Glu	Ser 375	Ala	Ile	Cys	Ala	Leu 380	Glu	Ala	Leu	Gln
Gly 385	Lys	Glu	Leu	Ser	Lys 390	Val	Gly	Ala	Pro	Ser 395	Thr	Val	Ser	Phe	Ala 400
Arg	Val	Leu	Pro	Met 405	Tyr	Glu	Gln	Pro	Leu 410	Asn	Val	Asn	Gly	Phe 415	Asn

Asn	Thr	Pro	Lys 420	Gln	Pro	Leu	Leu	Gln	Glu	Gln	Leu	Asn	His 430	Gly	Val
Leu	Asn	Tyr 435	Gln	Leu	Gln	Gln	Ser 440	Leu	Gln	Gln	Pro	Glu 445	Leu	Gln	Gln
Gln	Pro	Thr 450	Ser	Phe	Asn	Gln 455	Pro	Asn	Leu	Thr	Tyr 460	Cys	Asn	Pro	Thr
Gln 465	Asn	Leu	Ser	His	Leu 470	Gln	Leu	Ser	Ser	Asn 475	Glu	Asn	Glu	Pro	Tyr 480
Pro	Phe	Pro	Leu	Pro 485	Pro	Pro	Ser	Leu	Ser 490	Asp	Ser	Lys	Lys	Asp 495	Ile
Leu	His	Thr	Ile 500	Ser	Ser	Phe	Lys	Leu 505	Glu	Tyr	Asp	His	Leu 510	Glu	Leu
Asn	His	Leu 515	Leu	Gln	Asn	Ala	Leu 520	Lys	Asn	Lys	Gly	Val 525	Ser	Asp	Thr
Asn	Tyr 530	Phe	Gly	Pro	Leu	Pro 535	Glu	His	Asn	Ser	Lys 540	Val	Pro	Lys	Arg
Lys 545	Asp	Thr	Phe	Asp	Ala 550	Pro	Lys	Leu	Arg	Glu 555	Leu	Arg	Lys	Gln	Phe 560
Asp	Ser	Asn	Ser	Leu 565	Ser	Thr	Ile	Glu	Met 570	Glu	Gln	Leu	Ala	Ile 575	Val
Met	Leu	Asp	Gln 580	Leu	Pro	Glu	Leu 585	Ser	Ser	Asp	Tyr	Leu 590	Gly	Asn	Thr
Val	Ile	Gln 595	Lys	Leu	Phe	Glu	Asn 600	Ser	Ser	Asn	Ile	Ile 605	Arg	Asp	Ile
Met 610	Leu	Arg	Lys	Cys	Asn	Lys 615	Tyr	Leu	Thr	Ser	Met 620	Gly	Val	His	Lys
Asn 625	Gly	Thr	Trp	Val	Cys 630	Gln	Lys	Ile	Ile	Lys 635	Met	Ala	Asn	Thr	Pro 640
Arg	Gln	Ile	Asn 645	Leu	Val	Thr	Ser	Gly	Val 650	Ser	Asp	Tyr	Cys	Thr 655	Pro
Leu	Phe	Asn	Asp 660	Gln	Phe	Gly	Asn	Tyr 665	Val	Ile	Gln	Gly	Ile 670	Leu	Lys
Phe	Gly	Phe 675	Pro	Trp	Asn	Ser	Phe 680	Ile	Phe	Glu	Ser	Val 685	Leu	Ser	His
Phe 690	Trp	Thr	Ile	Val	Gln	Asn 695	Arg	Tyr	Gly	Ser	Arg 700	Ala	Val	Arg	Ala
Cys 705	Leu	Glu	Ala	Asp	Ser 710	Ile	Ile	Thr	Gln	Cys 715	Gln	Leu	Leu	Thr	Ile 720
Thr	Ser	Leu	Ile 725	Ile	Val	Leu	Ser	Pro	Tyr 730	Leu	Ala	Thr	Asp	Thr 735	Asn
Gly	Thr	Leu	Leu 740	Ile	Thr	Trp	Leu	Leu 745	Asp	Thr	Cys	Thr 750	Leu	Pro	Asn

Lys Asn Leu Ile Leu Cys Asp Lys Leu Val Asn Lys Asn Leu Val Lys
 755 760 765
 Leu Cys Cys His Lys Leu Gly Ser Leu Thr Val Leu Lys Ile Leu Asn
 770 775 780
 Leu Arg Gly Gly Glu Glu Glu Ala Leu Ser Lys Asn Lys Ile Ile His
 785 790 795 800
 Ala Ile Phe Asp Gly Pro Ile Ser Ser Asp Ser Ile Leu Phe Gln Ile
 805 810 815
 Leu Asp Glu Gly Asn Tyr Gly Pro Thr Phe Ile Tyr Lys Val Leu Thr
 820 825 830
 Ser Arg Ile Leu Asp Asn Ser Val Arg Asp Glu Ala Ile Thr Lys Ile
 835 840 845
 Arg Gln Leu Ile Leu Asn Ser Asn Ile Asn Leu Gln Ser Arg Gln Leu
 850 855 860
 Leu Glu Glu Val Gly Leu Ser Ser Ala Gly Ile Ser Pro Lys Gln Ser
 865 870 875 880
 Ser Lys Asn His Arg Lys Gln His Pro Gln Gly Phe His Ser Pro Gly
 885 890 895
 Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser Ser Asn Ser Arg
 900 905 910
 His Asn Ser Val Ile Gln Met Asn Asn Ala Gly Pro Thr Pro Ala Leu
 915 920 925
 Asn Phe Asn Pro Ala Pro Met Ser Glu Ile Asn Ser Tyr Phe Asn Asn
 930 935 940
 Gln Gln Val Val Tyr Ser Gly Asn Gln Asn Gln Asn Gln Asn Gly Asn
 945 950 955 960
 Ser Asn Gly Leu Asp Glu Leu Asn Ser Gln Phe Asp Ser Phe Arg Ile
 965 970 975
 Ala Asn Gly Thr Asn Leu Ser Leu Pro Ile Val Asn Leu Pro Asn Val
 980 985 990
 Ser Asn Asn Asn Asn Asn Tyr Asn Asn Ser Gly Tyr Ser Ser Gln Met
 995 1000 1005
 Asn Pro Leu Ser Arg Ser Val Ser His Asn Asn Asn Asn Asn Thr Asn
 1010 1015 1020
 Asn Tyr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn Asn Asn Asn
 1025 1030 1035 1040
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn
 1045 1050 1055
 Ser Asn Asn Asn Asn Asn Asn Asp Thr Ser Leu Tyr Arg Tyr Arg Ser
 1060 1065 1070
 Tyr Gly Tyr
 1075

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<400> 24
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  1                    5                10              15

Arg Ser Asn Ser Ser Ala His Asn Lys Thr Arg Gly Tyr Tyr Tyr His
          20                25              30

Gly Tyr Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn
      35                40              45

Gly Tyr Asn Gly Tyr Asn Gly His Val Tyr Val Arg Gly Asn Gly Cys
      50                55              60

Ala Ala Cys Ala Ala Cys Cys Cys Thr Met Asp Met
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<210> 25
<211> 380
<212> PRT
<213> Saccharomyces cerevisiae

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  20          25          30
Ser Asn Lys Asn Asn Asn Ser Asn Asn Ser Ser Ser Asn Asn Ser Asn
  35          40          45
Asp Thr Ser Ser Ser Lys Asp Gly Thr Ala Asn Asp Lys Gly Ser Asn
  50          55          60
Asp Thr Lys Asn Lys Lys Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn
  65          70          75          80
Ala Ser Ser Ala Gly Ser Gly Trp Thr Met Ser Ser Ser Ser Val Thr
  85          90          95
Thr Lys Arg Ser Lys Ala Asp Ser Lys Ser Cys Lys Met Gly Gly Asn
  100          105          110
Trp Asp Thr Thr Asp Asn Arg Tyr Gly Lys Tyr Gly Thr Val Thr Asp
  115          120          125
Lys Met Lys Asp Ala Thr Gly Arg Ser Arg Gly Gly Ser Lys Ser Ser
  130          135          140
Val Asp Val Val Lys Thr His Asp Gly Lys Val Asp Lys Arg Ala Arg
  145          150          155          160
Asp Asp Lys Thr Gly Lys Val Gly Gly Gly Asp Val Arg Lys Ser Trp
  165          170          175
Gly Thr Asp Ala Met Asp Lys Asp Thr Gly Ser Arg Gly Gly Val Thr
  180          185          190

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Thr Met Lys Asn Gly Cys Ser Trp Asp Lys Asp Ala Arg Asn Ser Thr
100 105 110

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<210> 27
<211> 286
<212> PRT
<213> Saccharomyces cerevisiae

<400> 27
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Glu Arg Arg Lys Ile Glu Ile Lys Phe Ile Glu Asn Lys Thr Arg Arg
  20          25          30
His Val Thr Phe Ser Lys Arg Lys His Gly Ile Met Lys Lys Ala Phe
  35          40          45
Glu Leu Ser Val Leu Thr Gly Thr Gln Val Leu Leu Leu Val Val Ser
  50          55          60
Glu Thr Gly Leu Val Tyr Thr Phe Ser Thr Pro Lys Phe Glu Pro Ile
  65          70          75          80
Val Thr Gln Gln Glu Gly Arg Asn Leu Ile Gln Ala Cys Leu Asn Ala
  85          90          95
Pro Asp Asp Glu Glu Asp Glu Glu Asp Gly Asp Asp Asp Asp
 100          105          110
Asp Asp Asp Asp Asp Gly Asn Asp Met Gln Arg Gln Gln Pro Gln Gln
 115          120          125
Gln Gln Pro Gln Gln Gln Gln Gln Val Leu Asn Ala His Ala Asn Ser
 130          135          140

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Leu	Gly	His	Leu	Asn	Gln	Asp	Gln	Val	Pro	Ala	Gly	Ala	Leu	Lys	Gln
145					150					155					160
Glu	Val	Lys	Ser	Gln	Leu	Leu	Gly	Gly	Ala	Asn	Pro	Asn	Gln	Asn	Ser
				165					170					175	
Met	Ile	Gln	Gln	Gln	Gln	His	His	Thr	Gln	Asn	Ser	Gln	Pro	Gln	Gln
			180					185					190		
Gln	Gln	Gln	Gln	Gln	Pro	Gln	Gln	Gln	Met	Ser	Gln	Gln	Gln	Met	Ser
			195				200					205			
Gln	His	Pro	Arg	Pro	Gln	Gln	Gly	Ile	Pro	His	Pro	Gln	Gln	Ser	Gln
	210					215				220					
Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Leu	Gln	Gln	Gln	Gln	Gln
225					230					235					240
Gln	Gln	Gln	Gln	Gln	Pro	Leu	Thr	Gly	Ile	His	Gln	Pro	His	Gln	Gln
				245				250						255	
Ala	Phe	Ala	Asn	Ala	Ala	Ser	Pro	Tyr	Leu	Asn	Ala	Glu	Gln	Asn	Ala
			260					265					270		
Ala	Tyr	Gln	Gln	Tyr	Phe	Gln	Glu	Pro	Gln	Gln	Gly	Gln	Tyr		
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<213> Saccharomyces cerevisiae															
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Ser	Lys	Gln	Ala	Lys	Glu	Glu	Lys	Ala	Lys	Ala	Val	Ser	Ser	Ser	Ser
			20					25					30		
Ser	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Glu	Ser	Glu	Ser	Glu
		35					40					45			
Ser	Glu	Ser	Glu	Ser	Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser
	50					55					60				
Glu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Glu	Ser	Glu	Ala	Glu	Thr
65					70					75					80
Lys	Lys	Glu	Glu	Ser	Lys	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Ser	Ser
				85				90						95	
Ser	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Glu
			100					105					110		
Ser	Lys	Glu	Ser	Ser	Ser	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp
		115					120					125			
Ser	Glu	Ser	Glu	Lys	Glu	Glu	Ser	Asn	Asp	Lys	Lys	Arg	Lys	Ser	Glu
	130					135					140				
Asp	Ala	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Ser	S					

Asn Glu Glu Thr Glu Glu Pro Ala Thr Ile Phe Val Gly Arg Leu Ser
165 170 175

Trp Ser Ile Asp Asp Glu Trp Leu Lys Lys Glu Phe Glu His Ile Gly
180 185 190

Gly Val Ile Gly Ala Arg Val Ile Tyr Glu Arg Gly Thr Asp Arg Ser
195 200 205

Arg Gly Tyr Gly Tyr Val Asp Phe Glu Asn Lys Ser Tyr Ala Glu Lys
210 215 220

Ala Ile Gln Glu Met Gln Gly Lys Glu Ile Asp Gly Arg Pro Ile Asn
225 230 235 240

Cys Asp Met Ser Thr Ser Lys Pro Ala Gly Asn Asn Asp Arg Ala Lys
245 250 255

Lys Phe Gly Asp Thr Pro Ser Glu Pro Ser Asp Thr Leu Phe Leu Gly
260 265 270

Asn Leu Ser Phe Asn Ala Asp Arg Asp Ala Ile Phe Glu Leu Phe Ala
275 280 285

Lys His Gly Glu Val Val Ser Val Arg Ile Pro Thr His Pro Glu Thr
290 295 300

Glu Gln Pro Lys Gly Phe Gly Tyr Val Gln Phe Ser Asn Met Glu Asp
305 310 315 320

Ala Lys Lys Ala Leu Asp Ala Leu Gln Gly Glu Tyr Ile Asp Asn Arg
325 330 335

Pro Val Arg Leu Asp Phe Ser Ser Pro Arg Pro Asn Asn Asp Gly Gly
340 345 350

Arg Gly Gly Ser Arg Gly Phe Gly Gly Arg Gly Gly Arg Gly Gly
355 360 365

Asn Arg Gly Phe Gly Gly Arg Gly Gly Ala Arg Gly Gly Arg Gly Gly
370 375 380

Phe Arg Pro Ser Gly Ser Gly Ala Asn Thr Ala Pro Leu Gly Arg Ser
385 390 395 400

Arg Asn Thr Ala Ser Phe Ala Gly Ser Lys Lys Thr Phe Asp
405 410

<210> 29
<211> 405
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 29
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Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
20 25 30

Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
35 40 45

Ile	Ala	Gly	Tyr	Val	Met	Asp	Asn	Arg	Ser	Gly	Ser	Asp	Ala	Ser	
50						55				60					
Gln	Asp	Arg	Ala	Ala	Gly	Gly	Gly	Ser	Ser	Phe	Met	Asn	Thr	Leu	Met
65					70					75					80
Ala	Asp	Ser	Lys	Gly	Ser	Ser	Gln	Thr	Gln	Leu	Gly	Lys	Leu	Ala	Leu
				85					90					95	
Leu	Ala	Thr	Val	Met	Thr	His	Ser	Ser	Asn	Lys	Gly	Ser	Ser	Asn	Arg
			100					105					110		
Gly	Phe	Asp	Val	Gly	Thr	Val	Met	Ser	Met	Leu	Ser	Gly	Ser	Gly	Gly
		115					120					125			
Gly	Ser	Gln	Ser	Met	Gly	Ala	Ser	Gly	Leu	Ala	Ala	Leu	Ala	Ser	Gln
						135					140				
Phe	Phe	Lys	Ser	Gly	Asn	Asn	Ser	Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly
145					150					155					160
Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly	Ser	Phe	Thr	Ala
				165					170					175	
Leu	Ala	Ser	Leu	Ala	Ser	Ser	Phe	Met	Asn	Ser	Asn	Asn	Asn	Asn	Gln
			180					185					190		
Gln	Gly	Gln	Asn	Gln	Ser	Ser	Gly	Gly	Ser	Ser	Phe	Gly	Ala	Leu	Ala
			195				200					205			
Ser	Met	Ala	Ser	Ser	Phe	Met	His	Ser	Asn	Asn	Asn	Gln	Asn	Ser	Asn
						215					220				
Asn	Ser	Gln	Gln	Gly	Tyr	Asn	Gln	Ser	Tyr	Gln	Asn	Gly	Asn	Gln	Asn
225					230					235					240
Ser	Gln	Gly	Tyr	Asn	Asn	Gln	Gln	Tyr	Gln	Gly	Gly	Asn	Gly	Gly	Tyr
				245					250					255	
Gln	Gln	Gln	Gln	Gly	Gln	Ser	Gly	Gly	Ala	Phe	Ser	Ser	Leu	Ala	Ser
				260				265					270		
Met	Ala	Gln	Ser	Tyr	Leu	Gly	Gly	Gly	Gln	Thr	Gln	Ser	Asn	Gln	Gln
				275			280					285			
Gln	Tyr	Asn	Gln	Gln	Gly	Gln	Asn	Asn	Gln	Gln	Gln	Tyr	Gln	Gln	Gln
						295					300				
Gly	Gln	Asn	Tyr	Gln	His	Gln	Gln	Gln	Gly	Gln	Gln	Gln	Gln	Gln	Gly
305					310					315					320
His	Ser	Ser	Ser	Phe	Ser	Ala	Leu	Ala	Ser	Met	Ala	Ser	Ser	Tyr	Leu
				325					330					335	
Gly	Asn	Asn	Ser	Asn	Ser	Asn	Ser	Ser	Tyr	Gly	Gly	Gln	Gln	Gln	Ala
				340				345					350		
Asn	Glu	Tyr	Gly	Arg	Pro	Gln	His	Asn	Gly	Gln	Gln	Gln	Ser	Asn	Glu
							360					365			
Tyr	Gly	Arg	Pro	Gln	Tyr	Gly	Gly	Asn	Gln	Asn	Ser	Asn	Gly	Gln	His
						375					380				

Asn Gln Asn Arg Tyr
405

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<210> 30
<211> 964
<212> PRT
<213> Saccharomyces cerevisiae
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Asp Thr Tyr Ser Asn Ile Pro Val Gly Arg Glu Ile Lys Ile Ile Leu
225 ———— 230 ———— 235 ———— 240

Cys Cys Val Leu Leu Arg Phe Tyr His Arg Pro Ser Phe Ile Arg Gln
260 265 270

Leu	Asp	Glu	Leu	Tyr	Glu	Thr	Asp	Pro	Asn	Asn	Tyr	Thr	Ser	Lys	Gln
		275					280					285			
Met	Gln	Phe	Leu	Pro	Leu	Cys	Tyr	Ala	Ala	Ile	Ala	Val	Gly	Ala	Leu
	290					295					300				
Phe	Ser	Lys	Ser	Ile	Val	Ser	Asn	Asp	Ser	Ser	Arg	Glu	Lys	Phe	Leu
305					310					315					320
Gln	Asp	Glu	Gly	Tyr	Lys	Tyr	Phe	Ile	Ala	Ala	Arg	Lys	Leu	Ile	Asp
				325					330					335	
Ile	Thr	Asn	Ala	Arg	Asp	Leu	Asn	Ser	Ile	Gln	Ala	Ile	Leu	Met	Leu
			340					345					350		
Ile	Ile	Phe	Leu	Gln	Cys	Ser	Ala	Arg	Leu	Ser	Thr	Cys	Tyr	Thr	Tyr
		355					360					365			
Ile	Gly	Val	Ala	Met	Arg	Ser	Ala	Leu	Arg	Ala	Gly	Phe	His	Arg	Lys
	370					375					380				
Leu	Ser	Pro	Asn	Ser	Gly	Phe	Ser	Pro	Ile	Glu	Ile	Glu	Met	Arg	Lys
385					390					395					400
Arg	Leu	Phe	Tyr	Thr	Ile	Tyr	Lys	Leu	Asp	Val	Tyr	Ile	Asn	Ala	Met
				405					410					415	
Leu	Gly	Leu	Pro	Arg	Ser	Ile	Ser	Pro	Asp	Asp	Phe	Asp	Gln	Thr	Leu
			420					425					430		
Pro	Leu	Asp	Leu	Ser	Asp	Glu	Asn	Ile	Thr	Glu	Val	Ala	Tyr	Leu	Pro
		435					440					445			
Glu	Asn	Gln	His	Ser	Val	Leu	Ser	Ser	Thr	Gly	Ile	Ser	Asn	Glu	His
	450					455					460				
Thr	Lys	Leu	Phe	Leu	Ile	Leu	Asn	Glu	Ile	Ile	Ser	Glu	Leu	Tyr	Pro
465					470					475					480
Ile	Lys	Lys	Thr	Ser	Asn	Ile	Ile	Ser	His	Glu	Thr	Val	Thr	Ser	Leu
				485					490					495	
Glu	Leu	Lys	Leu	Arg	Asn	Trp	Leu	Asp	Ser	Leu	Pro	Lys	Glu	Leu	Ile
			500					505					510		
Pro	Asn	Ala	Glu	Asn	Ile	Asp	Pro	Glu	Tyr	Glu	Arg	Ala	Asn	Arg	Leu
		515					520					525			
Leu	His	Leu	Ser	Phe	Leu	His	Val	Gln	Ile	Ile	Leu	Tyr	Arg	Pro	Phe
	530					535					540				
Ile	His	Tyr	Leu	Ser	Arg	Asn	Met	Asn	Ala	Glu	Asn	Val	Asp	Pro	Leu
545					550					555					560
Cys	Tyr	Arg	Arg	Ala	Arg	Asn	Ser	Ile	Ala	Val	Ala	Arg	Thr	Val	Ile
				565					570					575	
Lys	Leu	Ala	Lys	Glu	Met	Val	Ser	Asn	Asn	Leu	Leu	Thr	Gly	Ser	Tyr
			580					585					590		
Trp	Tyr	Ala	Cys	Tyr	Thr	Ile	Phe	Tyr	Ser	Val	Ala	Gly	Leu	Leu	Phe
		595					600					605			

Tyr	Ile	His	Glu	Ala	Gln	Leu	Pro	Asp	Lys	Asp	Ser	Ala	Arg	Glu	Tyr
610						615					620				
Tyr	Asp	Ile	Leu	Lys	Asp	Ala	Glu	Thr	Gly	Arg	Ser	Val	Leu	Ile	Gln
625					630					635					640
Leu	Lys	Asp	Ser	Ser	Met	Ala	Ala	Ser	Arg	Thr	Tyr	Asn	Leu	Leu	Asn
				645					650					655	
Gln	Ile	Phe	Glu	Lys	Leu	Asn	Ser	Lys	Thr	Ile	Gln	Leu	Thr	Ala	Leu
			660					665					670		
His	Ser	Ser	Pro	Ser	Asn	Glu	Ser	Ala	Phe	Leu	Val	Thr	Asn	Asn	Ser
		675					680					685			
Ser	Ala	Leu	Lys	Pro	His	Leu	Gly	Asp	Ser	Leu	Gln	Pro	Pro	Val	Phe
						695					700				
Phe	Ser	Ser	Gln	Asp	Thr	Lys	Asn	Ser	Phe	Ser	Leu	Ala	Lys	Ser	Glu
705					710					715					720
Glu	Ser	Thr	Asn	Asp	Tyr	Ala	Met	Ala	Asn	Tyr	Leu	Asn	Asn	Thr	Pro
				725					730					735	
Ile	Ser	Glu	Asn	Pro	Leu	Asn	Glu	Ala	Gln	Gln	Gln	Asp	Gln	Val	Ser
			740					745					750		
Gln	Gly	Thr	Thr	Asn	Met	Ser	Asn	Glu	Arg	Asp	Pro	Asn	Asn	Phe	Leu
		755					760					765			
Ser	Ile	Asp	Ile	Arg	Leu	Asp	Asn	Asn	Gly	Gln	Ser	Asn	Ile	Leu	Asp
						775					780				
Ala	Thr	Asp	Asp	Val	Phe	Ile	Arg	Asn	Asp	Gly	Asp	Ile	Pro	Thr	Asn
785					790					795					800
Ser	Ala	Phe	Asp	Phe	Ser	Ser	Ser	Lys	Ser	Asn	Ala	Ser	Asn	Asn	Ser
				805					810					815	
Asn	Pro	Asp	Thr	Ile	Asn	Asn	Asn	Tyr	Asn	Asn	Val	Ser	Gly	Lys	Asn
			820					825					830		
Asn	Asn	Asn	Asn	Asn	Ile	Thr	Asn	Asn	Ser	Asn	Asn	Asn	His	Asn	Asn
		835					840					845			
Asn	Asn	Asn	Asp	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn
		850				855					860				
Asn	Asn	Asn	Asn	Asn	Ser	Gly	Asn	Ser	Ser	Asn	Asn	Asn	Asn	Asn	Asn
865					870					875					880
Asn	Asn	Asn	Lys	Asn	Asn	Asn	Asp	Phe	Gly	Ile	Lys	Ile	Asp	Asn	Asn
				885					890				895		
Ser	Pro	Ser	Tyr	Glu	Gly	Phe	Pro	Gln	Leu	Gln	Ile	Pro	Leu	Ser	Gln
			900					905					910		
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Tyr Pro Ser Glu

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65 70 75 80

Leu Asn Ala Ser Leu Lys Gln Gly Leu Met Asp Ile Ala Ser Lys Gly
100 105 110

Asp Ile Val Ser Glu Asp Gly Leu Leu Pro Ser Lys Met Leu Met Asp
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Ala Asn Asp Thr Phe Leu Leu Glu Trp Trp Glu Ile Phe Gln Ser Leu
130 135 140

Phe Asn Gly Asp Leu Glu Ser Gly Tyr Gln Gln Asp His Asn Pro Leu
145 150 155 160

Arg Glu Arg Ile Ile Pro Ile Leu Pro Ala Asn Ser Lys Ser Asn Met
165 170 175

Pro Ser His Phe Ser Asn Leu Pro Pro Asn Val Ile Pro Pro Thr Gln
180 185 190

Asn Ser Phe Pro Val Ser Glu Glu Ser Phe Arg Pro Asn Gly Asp Gly
195 200 205

Ser Asn Phe Asn Leu Asn Asp Pro Thr Asn Arg Asn Val Ser Glu Arg
210 215 220

Phe Leu Ser Arg Thr Ser Gly Val Tyr Asp Lys Gln Asn Ser Ala Asn
225 230 235 240

Phe Ala Pro Asp Thr Ala Ile Asn Ser Asp Ile Ala Gly Gln Gln Tyr
245 250 255

Ala Thr Ile Asn Leu His Lys His Phe Asn Asp Leu Gln Ser Pro Ala
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Gln	Pro	Gln	Gln	Ser	Ser	Gln	Gln	Ile	Gln	Gln	Pro	Gln	His	Gln	
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Pro	Gln	His	Gln	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
	290					295					300				
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
305					310					315					320
Gln	Gln	Gln	His	Gln	Gln	Gln	Gln	Gln	Thr	Pro	Tyr	Pro	Ile	Val	Asn
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Pro	Gln	Met	Val	Pro	His	Ile	Pro	Ser	Glu	Asn	Ser	His	Ser	Thr	Gly
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Gln	Ser	Ser	Met	Phe	Ser	Asp	Gln	Gln	Arg	Phe	Phe	Gln	Tyr	Gln	Leu
	370					375					380				
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Gly	Arg	Phe	Asp	Asp	Met	Asn	Ala	Met	Lys	Met	Phe	Phe	Gln	Gln	Gln
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Ala	Leu	Gln	Gln	Asn	Ser	Leu	Gln	Gln	Asn	Leu	Gly	Asn	Gln	Asn	Tyr
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Gln	Pro	Leu	Tyr	Gln	Asn	Val	Ser	Ser	Ala	Met	His	Ala	Phe	Ala	Pro
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Gln	Gln	Gln	Phe	His	Leu	Pro	Gln	His	Tyr	Lys	Thr	Asn	Thr	Ser	Val
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Pro	Gln	Asn	Asp	Ser	Thr	Ser	Val	Phe	Pro	Leu	Pro	Asn	Asn	Asn	Asn
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Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Ser	Asn	Asn
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Thr	Pro	Thr	Val	Ser	Gln	Pro	Ser	Ser	Lys	Cys	Thr	Ser	Ser	Ser	Ser
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Lys	Val	Met	Lys	Ser	Lys	Lys	Leu	Glu	Gln	Asn	Gly	Asp	Ser	Ala	Ala
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Ser	Met	Asp	Thr	Glu	Thr	Phe	Asp	Ile	Phe	Asn	Ile	Gly	Asp	Phe	Ser
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Lys	Arg 210	Cys	Ser	Thr	Asn 215	Ser	Thr	Thr	Lys	Ser	Trp 220	Thr	Tyr	Lys	Asn
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Val 370	Asp	Ser	Ser	Asp	Tyr	Gly	Asn	Thr	Val	Lys	Asn	Ser	Ser	Asn	
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Lys	Asn	His	Asp	Thr	Met	Gly	His	Ser	Ser	Ser	Asp	Thr	Ser	Ser	Ser
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Asn	Asn	Lys	Ser	Asn	Ser	Ser	Thr	Asn	Thr	Val	Ser	Thr	Asn	Asn	Asn
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Tyr Asp Ser Lys Ser Lys Val Thr Asn Cys Asp His Lys Ala Ser Ser
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Ser	Lys	Trp	His	Arg	His	Asp	Lys	Lys	Met	Val	Lys	Lys	Ser	Arg	Tyr
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Arg	Lys	Arg	Met	Arg	Gly	Thr	Asp	Val	Ser	Ser	Ser	Asp	Asn	Ser	Lys
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Ser	Thr	Thr	Lys	Ser	Tyr	Val	Ser	Lys	Asn	Ser	Ala	Met	Asn	Asn	Asn
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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
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Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
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tgc	act	act	gga	aaa	cta	cct	ggt	cca	tgg	cca	aca	ctt	gtc	act	act		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
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Phe	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
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cgg	cat	gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	ggt	tat	gta	cag	gaa		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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180 185 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
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Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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005050:225650

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

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Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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<213> Artificial Sequence

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<210> 43
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<212> DNA
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 <212> PRT
 <213> Pichia pinus

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 180 185 190
 Ser Thr Val Lys Ala Pro Ile Val Thr Lys Lys Lys Glu Glu Glu Pro
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 Val Asn Gln Glu Ser Lys Thr Glu Glu Pro Ala Lys Glu Glu Ile Lys
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 Asn Gln Glu Pro Ala Glu Ala Glu Asn Lys Val Glu Glu Glu Ser Lys
 225 230 235 240

Val Glu Ala Pro Thr Ala Ala Lys Pro Val Ser Glu Ser Glu Phe Pro
 245 250 255
 Ala Ser Thr Pro Lys Thr Glu Ala Lys Ala Ser Lys Glu Val Ala Ala
 260 265 270

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Gly 465	Ile	Gly	Tyr	Ala	Lys 470	Asp	Asp	Ile	Ile	Tyr 475	Met	Pro	Val	Ser	Gly 480
Tyr	Thr	Gly	Ala 485	Gly	Leu	Lys	Asp	Arg	Val 490	Asp	Pro	Lys	Asp	Cys 495	Pro

Trp Tyr Asp Gly Pro Ser Leu Leu Glu Tyr Leu Asp Asn Met Asp Thr
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515 520 525

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530 535 540

Val Lys Lys Gly Thr Asn Leu Ile Met Met Pro Asn Lys Thr Pro Ile
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565 570 575

Phe Ser Gly Glu Gln Val Arg Leu Lys Ile Lys Gly Ile Glu Glu Glu
580 585 590

Asp Leu Gln Pro Gly Tyr Val Leu Thr Ser Pro Lys Asn Pro Val Lys
595 600 605

Thr Val Thr Arg Phe Glu Ala Gln Ile Ala Ile Val Glu Leu Lys Ser
610 615 620

Ile Leu Ser Asn Gly Phe Ser Cys Val Met His Leu His Thr Ala Ile
625 630 635 640

Glu Glu Val Lys Phe Ile Glu Leu Lys His Lys Leu Glu Lys Gly Thr
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Asn Arg Lys Ser Lys Lys Pro Pro Ala Phe Ala Lys Lys Gly Met Lys
660 665 670

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<212> DNA

<213> *Saccharomyces cerevisiae*

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gtttattcct ggcattcact aaatataatg gagcccgctt tttaagctgg catccagaaa 240

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<213> Artificial Sequence
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<212> PRT
<213> Saccharomyces cerevisiae

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Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
          35          40          45
Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
  50          55          60
Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
  65          70          75          80
Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
          85          90          95
-Leu-Ala-Thr-Val-Met-Thr-His-Ser-Ser-Asn-Lys-Gly-Ser-Ser-Asn-Arg-
          100          105          110
Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
          115          120          125

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<210>	51
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<212>	PRT

<400> 51

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<210> 52
<211> 534
<212> PRT
<213> Saccharomyces cerevisiae
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Glu	Tyr	Phe	Gly 180	Lys	Tyr	Gly	Thr	Val 185	Thr	Asp	Leu	Lys	Ile 190	Met	Lys
Asp	Pro	Ala 195	Thr	Gly	Arg	Ser	Arg 200	Gly	Phe	Gly	Phe	Leu 205	Ser	Phe	Glu
Lys	Pro 210	Ser	Ser	Val	Asp	Glu 215	Val	Val	Lys	Thr	Gln 220	His	Ile	Leu	Asp
Gly 225	Lys	Val	Ile	Asp	Pro 230	Lys	Arg	Ala	Ile	Pro 235	Arg	Asp	Glu	Gln	Asp 240
Lys	Thr	Gly	Lys	Ile 245	Phe	Val	Gly	Gly	Ile 250	Gly	Pro	Asp	Val	Arg 255	Pro
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Tyr His Pro Tyr Asn Arg
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<211> 36
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: primer

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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: primer

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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: primer

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<211> 40
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<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: primer

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<210> 58
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<400> 58
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<210> 59
<211> 34
<212> DNA
<213> Artificial Sequence
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<400> 59
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<220>
<223> Description of Artificial Sequence: primer

<400> 60
ggaccgcggg tagcggttct gttgagaaaa gttgcc 36

```
<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: primer

<400> 61
gaggatccat gcctgatgat gaggaagaag acgagg 36

```
<210> 62
<211> 26
<212> DNA
<213> Artificial Sequence
```

<223> Description of Artificial Sequence: primer

<400> 62
cggaattcct cgagaagata tccatc 26

24

34

35